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Description	Abk15699 Cotton fi Abz10246 Haematopo Abz10100 Haematopo	Adl17884 Human pho Abg75107 Anopheles Acf79720 Mosquito	Acf62816 Colon can Adb54318 Pretreate	Abz10246 Haematopo Acf62794 Colon can Adb54190 Pretreate	Abz10100 Haematopo Ab134155 Human imm Ab132326 Human imm	Aas61077 Human gen Ab132979 Human imm Abx46069 Bovine ES	Ads89278 Oligonucl Ads89552 Oligonucl Ab132357 Human imm
SUMMARIES	ABK15699 ABZ10246 ABZ10100	ADL17884 ABQ75107 ACF79720	ACF62816 ADB54318	ABZ10246 ACF62794 ADB54190	ABZ10100 ABL34155 ABL32326	AAS61077 ABL32979 ABX46069	ADS89278 ADS89552 ABL32357
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New fiber-specific beta-tubulin promoter from cotton for controlling gene expression in cotton fibers and creating transgenic plants, in particular cotton plants, having altered fiber characteristics.

The invention relates to a promoter that is cotton fibre-specific,

Claim 2; Fig 2; 30pp; English.

Abk39932 Human che		_	Abq67002 Human ang	Abl34358 Human imm	Aas46530 Tumour su	Abl32267 Human imm	Abq15588 Oligonucl			_	Abl32972 Human imm	Aat41852 cDNA enco	Abz10199 Haematopo	Aax33181 Base segu	Aax33182 Base segu	Aax33180 Cowpox vi	Aax33184 Base segu	Aaa70178 Plasmodiu	Abk31192 Signal tr	Abl70517 Chemicall	Aas61105 Human gen	Aas46591 Tumour su	Aas46787 Tumour su	Aas46735 Tumour su
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## ALIGNMENTS

449. .1433 /\*teg= a /note= "Cotton fibre-specific promoter. This sequence is specifically claimed in claim 3" Cotton; ds; CFTUB2; fibre-specific beta tubulin; transgenic. promoter; plant; anthocyanin gene; silk protein gene; cotton fibre strength; polyhydroxybutyrate. Cotton fibre-specific beta tubulin, CFTUB2, promoter fragment. Location/Qualifiers (MOLE-) INST MOLECULAR AGROBIOLOGY. ABK15699 standard; DNA; 1433 BP Liu J; 01-AUG-2000; 2000WO-SG000111. 01-AUG-2000; 2000WO-SG000111. (first entry) Li X, Cheng N, WPI; 2002-217120/27. Gossypium hirsutum. WO200210377-A1. 21-MAY-2002 07-FEB-2002. ABK15699; promoter Cai L, Key RESULT 1 **ABK15699** 

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promoter is fibre-specific in octon and controls specific gene expression at the transcriptional level in cotton fibres and is useful for improving cotton fibres to create new cotton varieties with high fibre quality and yield by gene manipulation. The promoter is useful caracteristics, and permits selective expression of a transgene in the characteristics, and permits selective expression of a transgene in the cotton fibre, permitting greater latitude in the types of transgenes cotton fibre, permitting greater latitude in the types of transgenes on in other parts of the cotton plants, include anthocyanin genes for coloured cotton, silk protein genes from silk worm or spiders for increased strength of cotton fibre, and biosynthesis of polyhdroxybutyrate in cotton fibre, and biosynthesis of polyhdroxybutyrate in cotton fibre for improved thermal properties and reate new cotton varieties with higher fibre quality and yield. The present sequence is the CFTUB2 promoter fragment
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the promoter of the cotton beta-tubulin gene CFTUB2. The
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100.0%; Score 985; DB 6; Length 1.
Best Local Similarity 100.0%; Pred. No. 4.3e-123;
Matches 985; Conservative 0; Mismatches 0; Indels
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differentiating between hematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute 1ymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cycosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the
                                                                                                                                               1348
1169 AACTACATTGTTACAGTTACTAAGCAAATCCCAATTTCAAAAATTCAATTTCCCAGGAAA 1228
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                                                      901 ATTICCGGAATICTIATICCTTTTATATTTTTCCTCTCCCAATTTCCCGTCACTTTCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between
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                                                                                                                                                            Score 107.4; DB 8; Length 8056;
Pred. No. 4.8e-06;
0; Mismatches 286; Indels 6;
                                                                                                                                Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                              Best Local Similarity 51.1%;
Matches 305; Conservative
                                                                                                                                                                 10.9%;
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                                                                                                                                                                                                                                                                                              112
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Haematopoietic cell proliferation disorder related DNA sequence #240
                                                                                                                                                                          Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
                                                                                                                                                                                               cytosine methylation state; gene; ds.
                                                                                             DNA; 8056
                                                                                                                                    (first entry)
                                                                                            ABZ10100 standard;
                                                                                                                                    16-JAN-2003
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                ABZ10100;
                                                                                RESULT
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7

Gaps

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Indels

Score 105.8; DB 8; Pred. No. 7.9e-06; 0; Mismatches 287;

Match 10.7%; Local Similarity 50.9%; hes 304; Conservative (

Query Match Matches

ઠ 셤 ò 셤 ò 요 ò 셤 . ☆ ద ò

Length 8056;

Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

111 114 171

52 AATTITITATTITACCTCCTGCCTAGATTCGTAAATACTATTGCATTTATCTCATTTCAT 112 TATTTATTTAATTTATTATTATTTGGATAAAAATTCTAATACTTTACTTTTAA TTTAAAAAGAATTTCAATTGCGTTTTTTTTTTAATTTTAATTTCTATACTAATTATA 291 

AAAGAATTTATTTAATTTATTATTTAGATAAAATTCTAATACTTTACTTTTT

172

351

411 412

353 ATTAAAAAAAAAAAAAACGAAATAAAATATTTATAATTTTAAATTTTAATATAT

352

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WO200277272-A2

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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG mucleotides within the target nucleic acid. AB209861 to AB21118 represent specifically claimed nucleotide sequences from the present invention. Onlygonocleotides from the present invention can be used: for invention. Oligonocleotides from the present invention can be used: for disorder haematopoietic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the maplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between the nucleotide sequences from the present method enables a highly specific classification of haematopoietic cell proliferative highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                          Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                    Pelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders allowing for improved and informed treatment of patients
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Β,
                                                                                                                                                                                                Mueller J;
e R, Leu E;
, Otto T,
                                                                                                                                                                                                Guetig D, Howe A, Muel
P, Grabs G, Lesche R,
Model F, Mueller V, Ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; SEQ ID NO 240; 117pp; English
                                                                                                                                                                                                Berlin K, Braun A, Distler J, (
Olek A, Piepenbrock C, Adorjan |
Lewin A, Lipscher E, Maier S, 1
                                               26-MAR-2002; 2002WO-EP003401
                                                                                                 26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                         Ziebarth H;
                                                                                                                                                   (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                WPI; 2003-018942/01
03-OCT-2002.
                                                                                                                                                                                                                                                                            Schwope I,
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The invention relates to a compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding phosphotyrosyl phosphatase activator (PPTA), that specifically hybridises with the nucleic acid molecule encoding phosphatase activator and inhibits the expression of phosphotyrosyl phosphatase activator, i.e. and antisense of phosphotyrosyl phosphatase activator in cells the expression of phosphotyrosyl phosphatase activator in cells or tissues, a method of tracting an animal having a disease or condition associated with phosphotyrosyl phosphatase activator and a method of screening for an antisense compound. The disease or condition associated can antisense compound. The disease or condition is a hyperproliferative an antisense compound. The disease or condition is a hyperproliferative can exclose or isonate or according phosphotyrosyl phosphatase activator. The compound can also be useful in modulating the function of nucleic acid molecules encoding phosphotyrosyl phosphatase activator. The can also be used as research tools and diagnostics. It can also be used as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues. The compound can also be used
467
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                                                                                                                                        527
                                                                                                                                                                                                                532
                                                                                                                                                                                                                                                                                    TAATCTCACCCTCCATTAATGCATATTATTAATTTTTTGTTCGATACTTCTTATTTCACTC 587
                                                                                                                                                                                                                                                                                                                                                        TAAAATTAAAATTTATTAATTATTAAAACGTTTTAATAAATTTATTATTAATA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                    644
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                                                                ACTCTCATCATTAAATTTAATCTTACCATAATTAAAAATTGTGAGGACAATTATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACTTATTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, ds, antisense, phosphotyrosyl phosphatase activator, PTPA,
hyperproliferative disorder, developmental disorder; infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human phosphotyrosyl phosphatase activator, PTPA, gene
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ADL17884/C
ID ADL17884 standard; CDNA; 158001 BP
XX
AC ADL17884;
XX

O6-MAY-2004 (first entry)
XX
Human phosphotyrosyl phosphatase a
XX
Human; ds; antisense; phosphotyrosy
KW
Hyperproliferative disorder; devel
KW
Hyperproliferative disorder; devel
KW
Hyperproliferative disorder; devel
KW

XX
Homo sapiens.
XX

US2004023906-A1.
XX

O5-FEB-2004.
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O5-FEB-2004.
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O5-FEB-2004.
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MD Dean NW, Dobie KW;
XX

C1S1S-) ISIS FHARM INC.
XX

MPI; 2004-132607/13.
XX

New antisense compound targeted to proportyrosyl phosphatase activat phosphotyrosyl phosphatase activat phosphotyrosyl phosphatase activat disorders.
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New antisense compound targeted to proposphotyrosyl phosphatase activat contained phosphotyrosyl phosphatase activat disorders.
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New antisense compound targeted to proposphotyrosyl phosphatase activat disorders.
XX

New antisense compound. The disease of phosphotyrosyl phosphatase activat disorder or developmental disorder and sparamectatical carrier or disorder or developmental disorder antisense compound. The disease contains and the phosphotyrosyl phosphatase activat hosphotyrosyl phosphatase activat antisense compound animal having can antisense compound animal having call molecules encoding phosphotyrosyl phosphatase activat hosphotyrosyl phosphatase activat hosphotyrosyl phosphatase activat hosphotyrosyl phosphatase activat hosphotyrosyl phosphatase activated an antisense compound animal having be used as tools in difference can also be used as tools in difference compound as tools in difference compound animal having the service of elucidate expression patents of enclaster of elucidate expression patents of enclaster of elucidate expression patents of enclaster of elucidate expression pat
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                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645
                                                                                    Sequence 158001 BP; 34764 A; 40497 C; 41696 G; 40433 T; 0 U; 611 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mosquito; olfactory gene; arrestin 1; pest control; olfaction; gene; ds.
          phosphatase activator, preferably hyperproliferative disorder or developmental disorder. The compound can also be used as prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. present sequence is the human PTPA gene which is a target for the antisense oligonucleotides of the invention.
                                                                                                                                                                                                              TATITATITIAAIITATITITATATITIGGATAAAAAITCITAATACITITITITITAA
                                                                                                                                                                                                                                                                                                                                                                                                                                    52 AATTITITATITITACCICCTGCCTAGATICGIAAAIACTATIGCAITITAICTCATITCAI
                                                                                                                                                                                   TATAAAAATTCTGATCGGATTAGTGTGTGTCAAAGTCAAGTCACATGAATTTTGTTGGA
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treating diseases or conditions associated with phosphotyrosyl
                                                                                                          Length 158001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.
                                                                                                          tch
al Similarity 49.7%; Pred. No. 7.7e-06;
297; Conservative 0; Mismatches 297; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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456 CACAACAATTACACTCCTCATTAAATTTAAATCTTATTACCATAATTAAAATTGTGAGG 515
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/*tag= 1
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1994. .2106.
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1602. .1702
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1887. .1993
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/*tag= k
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/number= 1
1. .485
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/product= '
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'number= 2
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                                                                                                                                                                                                                      The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of [G1] with at least 20 consecutive residues. Also described: (1) an isolated polymucleotide comprising: (3) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (D) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising capabiae olfaction polypeptide; or (D) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising capabiae 1142, 1236, 1194, 1176, 474 or 1206 mucleotide sequence (see ABG75102 to ABG75105 and ABG75110 to ABG75113) (S2), or its complement; and (2) a method for identifying an agent that binds to mosquito olfaction molecule; (b) contacting a test agent with the isolated mosquito olfaction molecule; (c) detecting specific binding compound. The mosquito olfaction molecules are useful for mosquito management, i.e. controlling this pest and disease vector. A method from the present invention of screening for substances that condulate arrestin-odourant receptor interaction is useful for identifying pest control agents. The present sequence represents Anopheles gambiae codourant receptor 2 genomic DNA from the present invention. N.B. The centering given in figure 4a are tentative and do not directly encode SEQ ID NO:6 (ABP52835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2678 ATTAATTTATTATTAATTATTATTATTGTTATTCATTATTATTATACATT--ATTATCAT 2735
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                                                                                                                                        mosquito management, i.e. controlling the pest and disease vectors, or for identifying pest control agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4985 BP; 1319 A; 1058 C; 990 G; 1618 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 266; Indels
                                                                                                                                                                                                   Disclosure; Fig 4a; 96pp; English.
 28-JAN-2002; 2002WO-US002549.
                       26-JAN-2001; 2001US-0264649P.
24-JAN-2002; 2002US-00056405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 276; Conservative
                                                             (UYVA-) UNIV VANDERBILT
                                                                                                             WPI; 2002-627421/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                           P-PSDB; ABP52835.
                                                                                      Zwiebel LJ;
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Mosquito; odorant receptor 2; olfaction; insecticide; antimalarial; gene;
                                                                                                                                   576 CTTATTTCACTCCTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACT
                                                     "Odorant receptor 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "contains introns"
03. .798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mosquito odorant receptor 2 genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                    ACF79720 standard; DNA; 4985 BP
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                             The present sequence is that of genomic DNA encoding a novel mosquito olfaction molecule, odorant receptor 2. A cDNA sequence for odorant receptor 2. A cDNA sequence for odorant receptor 1 is given in ACT9719. The invention provides 9 novel mosquito polypeptides and the nucleic acids encoding them. These are odorant receptor molecules 1-7 and arrestins 1 and 2. The odorant receptors function in a ligand-induced signal transduction pathway for the activation of mosquito olfaction. Arrestin functions to inhibit the activated signal transduction ascade. Thus, the odorant receptors act as an 'on' switch, and arrestin as an 'Off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere with the operation of the mosquito olfactory system, particularly compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate sources of bloodmeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reduce
                                                                                                                                                                                                                                      New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 ATTTATCTCATTTCATTTATTTAATTATTTTATTTTTGGATAAAATTCTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATACTTTACTTTTTTTAAAAGAATTTCAATTGCGTTTTTTCTTAATTTAGTTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 10.6%; Score 104.4; DB 10; Length 4985; Local Similarity 50.7%; Pred. No. 1.3e-05; es 276; Conservative 0; Mismatches 266; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4985 BP; 1319 A; 1058 C; 990 G; 1618 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                              Disclosure; Fig 4a; 101pp; English
                                               /*tag= 0
                                                                                                                                                       08-MAR-2002; 2002US-00094240
/number= 6
2107. 3459
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3460. 4985
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3562. 4985
                                                                                                                                   10-MAR-2003; 2003WO-US007174
                                                                                                                                                                           (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                    WPI; 2003-722331/68.
                                                                                            WO2003076590-A2
                                                                                                                 18-SEP-2003,
                                                                                                                                                                                               Zwiebel LJ
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the present into present the second of the present into present in the present into present in the present into present into the present into present into present into present into the paper second of the progesterone receptor, myoglobin, pona, cdc2, c-erB2, p53, and/or CRB4, which comparises contacting the target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides, and determining from the methylation status of the CpG dinucleotides, and determining from the methylation state and/or single nucleotide polymorphisms of the Cycsine methylation state and/or single nucleotide polymorphisms (SNP) of a corresponding genomic DNA by analysis of a chemically presenced genomic DNA is useful for the determination of the methylation status of a corresponding genomic DNA and/or detection of the methylation status of a corresponding genomic DNA and/or detection of the methylation status of a corresponding genomic DNA and/or detection of the methylation status of a corresponding genomic DNA are also useful for the characterisation, classification, diagnosis and differentiation of colon cell proliferative disorders. ACR63278 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                      575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a method for determining the methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53; progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG; characterisation; classification; diagnosis; differentiation; colon cell proliferative disorder; gene; ds.
    576 CTTATTTCACTCCTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACT
                                                                                                                                                                                 ACAATTATTTTTAATCTCACCCTCCATTAATGCATATTATTAATTTTTTGTTCGATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colon cancer analysis related genomic DNA SEQ ID NO:65.
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                                                                                                                                                                   587 CCTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACTTATTCACTATT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
                                                          ATTTATTTAATTATT - - TTATATTTGGATAAAATTCTAATACTTTACTTTTTTA
                                                                                                                                     TTTTAAAAAGAATTTCAATTGCGTTTTTTCTTAATTTAGTTTTAATTTCTATACTAATTAT
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                                                                                        TITITIATITIAATGITGTCAATAATATITITIAATTAA--AATITICAGCACAACTTACA
                                                                                                                                                                                                                                                            469 CTCTCATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACAATTATTTTT
                               Gaps
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Sequence 8222 BP; 2010 A; 0 C; 1769 G; 4443 T; 0 U; 0 Other;
              Score 102.4; DB 8; Length Pred. No. 2.2e-05; 0; Mismatches 286; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pretreated genomic DNA region 242
                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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               Query Match
10.4%;
Best Local Similarity 51.5%;
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one seares to a series of reagents, where the reagent or series of dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic acivity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide polymorphisms. The current sequence is that of the pretreated genomic DNA region of the invention. This sequence is not shown within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350
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                                                                                                                                                                                                         Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
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                                                         В.
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                                                         Becker E,
                                                         Nimmrich I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification but is taken from Wipoweb.
                                                                                                                                                                                                                                                                                                                                                                  Claim 32; SEQ ID NO 374; 74pp; English
                                                         Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.5%;
Matches 310; Conservative
(EPIG-) EPIGENOMICS AG.
                                                         Burger M,
                                                                                         Schmitt A;
                                                                                                                                               WPI; 2003-731620/69
                                                         Adorjan P,
Rujan T, S
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                                                                                 473 CATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACAATTATTTTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AAATTCTGATCGGATTAGTGTGTGTCAAAGTCAAGTCACATGAATTTTGTTGGAGAAA
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Score 101.6; DB 8;
                     Pred. No. 2.9e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACF62794 standard; DNA; 8222
                       al Similarity 49.4%;
291; Conservative
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    Query Match
Best Local S
Matches 291
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                                              Detecting and differentiating between hematopoietic cell proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, comprises contacting a target nucleic acid with a reagent the distinguishes between methylated and non-methylated CpG dinucleotides.
         CCTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACTTATTCACTATT
                                                                                                                                                                                                                                                                                                                                                                                       Haematopoietic cell proliferation disorder related DNA sequence #386
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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G, Lésche R, Leu E;
Mueller V, Otto T, 1
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P, Grabs G
Model F, N
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Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                            ABZ10246 standard; DNA; 8056 BP
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Human, colon cancer, oestrogen receptor, myoglobin, p21; p27; p16; p53; progesterone receptor, pcna, CEA, cdc2, c-erbB2; methylation, CpG; characterisation, classification, diagnosis, differentiation, colon cell proliferative disorder, gene, ds.
Colon cancer analysis related genomic DNA SEQ ID NO:43.
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Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation state and/or single nuclectide polymorphisms (SNP) of a corresponding genomic DNA by analysis of a chemically pretreated genomic DNA. The pretreated genomic DNA is useful for the determination of the methylation status of a corresponding genomic DNA and/or detection of SNPs. The methods and pretreated genomic DNA are also useful for the characterisation, classification, diagnosis and differentiation of colon cell proliferative disorders. ACF62752 to ACF63278 represent sequences
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                                                                                                                                                                           The present invention describes a method for determining the methylation status of CpG dinuclectides within the genes for oestrogen receptor, p21, p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erB2, p53 and/or CBA, which comprises contacting the target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides, and determining from the methylation status of the CpG positions the presence of a colon cancer. A set of oligomers or peptide nucleic acid (PNA)-oligomers can be used as probes for determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITTAAAAAGAATITCAATTGCGTTTTTTCTTAAITTAGTTTTAATTCTATACTAATTAT 290
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                                                                    Determining methylation status of CpG dinucleotides using modified genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the characterization, grading, staging and/or diagnosis of colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 AATCTCACCCTCCATTAATGCATATTATTAATTTTTGTTCGA--TACTTCTTATTTCACT
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                                                                                                                                             Claim 22; Page 81-83; 219pp; English.
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Taubert
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Model F,
                                    WPI; 2003-256600/25
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 Distler J,
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The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of casents, distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful or detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide colon methylation state or single nucleotide solvention. This sequence is that of the pretreated genomic DNA region of the invention. This sequence is not shown within the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
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                                                                                                                                                                                                                                                                                  cytostatic; cancer; adenoma; carcinoma; cytosine methylation state;
                                                                                                                                                                                                                                                              proliferative disorder; non methylated CpG dinucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 32; SEQ ID NO 246; 74pp; English
                                                                                                                                                                                                                               Pretreated genomic DNA region 114.
                                                                                                                        ADB54190 standard; DNA; 11222 BP.
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nes 309; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmitt A;
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Rujan T, S
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                                                                                                                                             Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, Pelet
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least i gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder callated sequences and their complements; and as primers for the ample of the nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of the mematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
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RESULT 13

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neuroclibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                  system disease; cytosine methylation; antiasthmatic;
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Pred. No. 0.00014;
0; Mismatches 223; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
                                                                                                                  Human immune system associated gene SEQ ID NO: 2128.
                    ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin
                    standard; DNA; 15548
                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-01032529.01-SEP-2000; 2000DE-01043826.
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9.8%;
Best Local Similarity 53.7%;
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                    ATTTATTTAATTATTTTATATTATTGGATAAAATTCTAATACTTTAGTTTTTTTAAA
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  Length 6109;
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                          Indels
Score 95.4; DB 6;
Pred. No. 0.0002;
0; Mismatches 296;
9.78;
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2000DE-01019173,
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             Best Local Similarity 49.7
Matches 296, Conservative
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07-APR-2000;
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                                                                                   nucleic acid sequences from chemically modified genes associated with a regulation, useful for analyzing cytosine methylations for diagnosis therapy of diseases e.g. severe combined immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                  53 ATTITITATITIACCICCIGCCIAGATICGIAAATACTATIGCATITATCICATITICATT 112
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                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 95.4; DB 6; I
49.7%; Pred. No. 0.0002;
ative 0; Mismatches 296;
                                                                                                                            Claim 1; SEQ ID NO 33; 26pp; English.
                                               Berlin K;
30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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                                               Piepenbrock C,
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nes 296; Conserva
                             EPIGENOMICS
                                                                  WPI; 2002-017470/02
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Search completed: March 14, 2005, 23:50:30 Job time : 575 secs

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Run on:

Sequence:

Searched:

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PAT 01-MAR-2002
AF201115 Dugesia p
CR352215 Danio rer
CR62608 Danio rer
D31785 Pichia cana
AK599046 Sequence
CR374519 Danio rer
CR374519 Danio rer
AC022281 Homo sapi
AX598900 Sequence
AC136557 Homo sapi
AC109994 Homo sapi
AC109994 Homo sapi
AC109994 Homo sapi
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AC136511 Human DNA
AL672277 Human DNA
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AL672277 Homo sapi
CR356223 Danio rer
AC016543 Homo sapi
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Arabidopsis sp.
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cai, L. I., Li, X., Cheng, N. and Liu, J.W. Isolation and characterization of a fiber-specific g(b)-tubulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGTGACCAGTGGTTGGAGAGAGGTCTACCGATTGGTCAAGTGGCACCAATTTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Patent: WO 0210377-A 2 07-FEB-2002;
Institute of Molecular Agrobiology (SG)
Location/Qualifiers

    1433
    /organism="Arabidopsis sp./mol_type="unassigned DNA"
/db_xref="taxon:29726"

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   AF201315
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CR356223
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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AF487511 Cossypium
AC125567 Rattus no
AL034556 Plasmodiu
CR391376 Danio rer
AC117140 Rattus no
AE014832 Plasmodiu
CR847965 Danio rer
CR847965 Danio rer
CR382399 Plasmodiu
CR536620 Danio rer
CR382399 Plasmodiu
CR536620 Danio rer
CR382399 Danio rer
AC111404 Rattus no
EX847875 Zebrafish
Continuation (13 o
CR392343 Danio rer
AC111404 Rattus no
EX842571 Zebrafish
                                                                                                             March 14, 2005, 20:13:50 ; Search time 4297 Seconds (without alignments) 11107.374 Million cell updates/sec
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                  version 5.1.6
- 2005 Compugen Ltd.
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AFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQDATADDEESYEEEEEFRARR
                         Li,X.B., Cai,L. and Liu,J.W.

Li,X.B., Cai,L. and Liu,J.W.

Direct Submission and Cotton
Submitted (25-FBB-2002) Latoratory of Plant Reproduction and Cotton
Biotechnology, Institute of Molecular Agrobiology, 1 Research Link,
NUS, Singapore 117604, Republic of Singapore
Location/Qualifiers

1. 5765

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| Corganism = Gossypium hirsutum"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossyptum.
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Li, X.B., Cai, L., Cheng, N.H. and Liu, J.W.
Li, X.B., Cai, L., Cheng, N.H. and Liu, J.W.
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Plant Physiol. 130 (2), 666-674 (2002)
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                                                                              AC125567 170627 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-9H22, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                        1073 ATCTGGAAAGGCCACCGTCCAGGCTGTCCAACCACACTTTGCCACGTCATCAATTCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAAACGTCCGTTACTAACCGACCTAAAACCCAGCTCAACCTGCCGTCAATTAACGGAA
                                                                                                                                                            TTAACCCAATTTTGAACTGTTATAATTTCTTAACTTATTCACTATTGTGGCTCTGGGTCC
                                                                                                                                                                                                                                                                      ATCTGGAAAGGCCACCGTCCAGGCTGTCCAACCACATTGCCACGTCATTCCAGT
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23096537.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rad). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangua, P., Martin, R., Martinez, B., Mangua, P., Martin, R., Martinez, B., Mangua, P., Martin, T.Z., Meenen, E., Malbaue, P., Martin, R., Menen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Morris, R., Murdhy, M., Nark, M., Nark, M., Nark, M., Nark, M., Nark, M., Nark, M., Nark, M., Narker, D., Navlon, M., Nouven, N., Norris, S., Parks, K., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perez, A., Perez, M., Regier, M. A., Reigh, R., Reilly, M., Ren, Y., Reuter, M., Rose, R., Ruiz, S.J., Reilly, M., Ren, Y., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sneet, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheet, M., Strong, R., Sutch, M., Tabor, P., Taylor, T. Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, T. Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Wang, O., Wang, C., Wallsen, M., Strong, R., Waler, S., Walker, S., Yon, V., Williams, G., Willson, M., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Weit, S., Mith, P., Nierer, S., Marter, S., Dunn, D., von Niederhausern, A., Weiss, R., Weit, S., Mith, P., Smith, H.O., Nierer, S., Weit, S., Dunn, D., von Niederhausern, A., Weiss, R., Weit, S., Mith, P., Smith, H.O., Nierer, S., Weit, S., Dunn, D., von Niederhausern, A., Weiss, R., Weit, S., Mith, S., Weit, S., Mer, S., Dunn, S., Smith, H.O., Nierer, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Weit, S., Wei
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170627)
Rat Genome Sequencing Consortium.
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Consensus quality: 162619 bases at least Q40
Consensus quality: 164392 bases at least Q30
Consensus quality: 165269 bases at least Q20
Estimated insert size: 169231; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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Center clone name: CH230-9H22
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2 (bases 1 to 170627)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                       Score 119.2; DB 2; Length 170627;
Pred. No. 6.4e-07;
0; Mismatches 293; Indels 0;
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                                                                           1 109158: contig of 109158 bp in length 1159 109258: gap of unknown length 1259 110280: contig of 1022 bp in length 1381 110380: gap of unknown length 1381 111540: contig of 1160 bp in length 1541 11640: gap of unknown length 1541 170527: contig of 58987 bp in length.
                                                                                                                                                                                                  /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                         1. .1284
/note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                     end_sequence:BH341988"
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/note="clone boundary
                                                                                                                                                                                                                                           clone="CH230-9H22"
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Best Local Similarity 50.2%;
Matches 295; Conservative
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note="synonym: PFC0575w"
join(322. .603,826. .1023,1197. .1301,1458. .1533,1696. .2942)
gene="WAL3P5.1"
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gene="MAL195.1"
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
INV 29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mutter, S., Skelton, T., Quail, M.A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and Barrell, B.G.
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                            Plasmodium falciparum MAL3T5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179 AL844502
AL0134556.4 Gl:23477013
HTG; centromere; CTRP protein; initiation factor E4;
Serine/threonine protein phosphatase.
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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/organism="Plasmodium falciparum 3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 400 (6744), 532-538 (1999)
99376085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="genomic DNA"
/isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="MAL3P5"
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gene

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/translation="MITYSSYFDDYVEDLARYLHKIKHSIYNITNKEDYNKTREYIFE
DMTKKYKEOVDFLAESERRAQDIEDIGYTIMSELNSQRSAILRTKHHTDETRQEQNRV
KRMLLIIANIGNSFPLF"
                                                        /gene="PFC0582c"
complement(join(10024. .10044,10320. .10336,10397. .10445,
10613. .10674,10773. .10798,10929. .10999,11157. .11237,
11453. .11515,11715. .11767,11950. .12040))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Signal peptide predicted by SignalP 2.0 HPM (Signal peptide probabilty 0.921, signal anchor probability 0.075) with cleavage site probability 0.888 between residues 20 and 2, revised: changed donor in comparison with P.
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KRGZIYNKKYKTYIEKRKYNYIKKGKNNNSYFSYCNYYKNNDVNNYTYXNYIND
KNKLKEYYBKIKNHYIKKKKKIFSLKESQNKRNBKKKKYFFINFTSFHDIKDIKONIIKVLE
NIDYIENNIIYSYIKSFKRTPPITKIYLGFFLLSVLIHMNKNVYKLILFDFNKIFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEIWRLFTPYLYIGNLYLQYILMFNYLNIYMSSVEISHYKKPEDFLIFLTFGYISNLL
FTIWANWYNENIMNVKLYIHNFKNFFIKDCVSKYTSRSSTNNNSNNINSNNKSSNNNN
HYNNSKNIDIKKEQYNHLGYVFSTYILYYWSRINEGTLINCFELFFIKAEYVPFFFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KII EEKLSSFKIQEI VNILEVSLNKNI IINKKY PHFLNQEKINIRNY INIYVNINKIY
LNDEEENTSHCILKI KNDNKKDILYHDHMKFLYNLMNBIIYRNDLLLMMKQIILLLYGL
KFNNFMFLQFEKIILKRFICLPKKEIQKIGKEEIMFLYQYFFVRTCLFNELKKQNNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISODEYENYIYISDKYNESAKLDNSYNMPSNLKEKNTNHHGGKDNTLDLYIHDDLFYM
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INNNNNNNNNNNNIYIYDTNIQTVNKYYSCTHNNVIKNFTNDNYPNSTIRNQHPNDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUNDVFFYNKKLMVVDSIDFEYELTCYNLYLDIYKIVCLKLLTLLKNHKLSCLQSID
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QDLKKIEMMVYDDNLTFKFYKLFKNILSINVKRYVQNCNSYNKYEMMTHNNLNKNEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
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/note="synonym: PPC0590c"
complement(join(13653. .17754,18005. .19353))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (13653. .17754,18005. .19353))
                  .11515,11715. .11767,11950. .12040))
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                                                                                                                                                                                                                                                                                                             /gene="PFC0582c"
/note="Revised: new gene prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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thes 288;
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/product="hypothetical_protein"
/protein_id="CAB38986.3"
/db_xref="G1:23477015"
/db_xref="UniProt/TrEMBL:097275"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="hypothetical protein"
/protein_id="CAB90286_1"
/db_xref="GI:7711067"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113.2; E
Pred. No. 4.4e-
0; Mismatches
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larity 52.3%;
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hes 319; Conserv
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3302. .8858,8568. .8641,8713. .8812,8924. .9006,9122. .9258,
9369. .9550,9613. .9838)
/gene="PPCO581w"
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LKVKDEEIVSKKNNFSFSALSNDSNSVTKKYIVDLTLLDNIIESETKKNFASVGKVVV
TLKEKKKINNRLLLSKEKYPNMQWWDMKEKRIHITFYTINLFFLLSLSHRYHDSV
QNFLKEEKNNSOPLODIDEDERVENSTERAKKGSEYNKDDEEL"
complement (join (10024 . 10044, 10320 . 10336, 10337 . 10445, 10613 . 10674, 10773 . 10798, 10929 . 10999, 11157 . 11237,
                                                                                                                                                                                                                                                                                                                                                               NINNLTRIKQVTHKKKSNEFTKENIKQILLHCVFSKIDFKIINNLSYIIKHFOMSNIT
VHSILNQISEKVKEKKDAENYLALHLFLLKDENITLFSMMHIMDFFKSKOKVIECIRD
IKKRIYECVGDLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDDLYFNYHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLRCFTWKLNIERNWKNI IRSNYDNINNDI SIDKOMYMNPIDVNINNISLDEKIKEQ
BERDDDENIKERLKOTYEQCLENDNI IKYIEEDOPLYNINDUSNINDNNNINITWKUK
HKIKOTYNDDDDYDYEEEDLUJOKNIDDY IKYNTIGMKSLEBFKNOPIEQADIEFO
NPLSNYNLDQHGRVKSNDENTKSTEHIKNKNITINKGYDTELIQNQMENNEIKKORIDEN
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NNNIVNGDIKNNNII PKKKYNLFESSIISYFYIKDIYEYNYKLRLYYIYDDLIKKFCR
YFLKMNEHINRKLYKMKRAFHYYIYNFDQFIINNYYHIIHKKNIHKIHIHLKQCKDKE
                                                                                                                                                                                                                                        /trānslation="MYLKNVYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFL
RSPQIYRKRFKRSRIKNVSFKKKQKKPLFLFENLKKGFSFLGFWRNQYDQKYIDDVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I SNDI SNNEINI I KLIKKLNQSDEDINLTSDLI YERLRTKVLWYI QXI EYLKFKY QYDI
I NEQYPI I KNEKTVLDLLNYGYKI VMSPDVDNSLPEKTKI DSI PNEKDKNNQMENQKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Signal peptide predicted by SignalP 2.0 HPM (Signal peptide probability 0.635, signal anchor probability 0.287) with cleavage site probability 0.594 between residues 21 and 22; CDS conserved in p. knowlesi and P.yoelii"
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/translation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
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QKIFHIYFANBQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDIVKFKDLYYCMINNINNIFSYIHKVDHNECVYRIFKAYNKILLYEYNYLNEKENIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jóin(7669. 7717,7800. 7829,7912. 7940,8064. 8106,
8302. 8368,8568. 8641,8713. 8812,8924. 9006,9122.
9369. 9505,9613. 9838)
                                                                                                                                                                                            xref="UniProt/TrEMBL:097258"
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/gene="MAL3P5.2"
/note="synonym: PFC0580c"
complement (3354. .6644)
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//Jecusionally annotated as Plasmodium falciparum; //Jecusionserved hypothetical protein but pfam match and other evidences suggest that it is a putative deoxyribonuclease; earlier start site possible to make a 412 aa protein pfam match to entry PF01026 TatD_DNase, TatD related DNase, score 117.30, E-value 2.9e-31 Similar to Plasmodium falciparum conserved hypothetical protein, upf0006 family malipa.01 SWALL:Q90006 (EMBL:AL031746) (412 aa) fasta scores: E(): 3.7e-150, 100% id in 412 aa, and to Saccharomyces cerevisiae putative deoxyribonuclease ybl055c ybl055c or ybl0512 or ybl0511 SWALL:PB2 YEAST (SWALL:P34220) (418 aa) fasta scores: E(): 2.5e-19, 30.47% id in 397 aa"
                                                                                                                                                                                                                                    Complement (join (201. .257,455. .586,748. .804))
/ Gene="PRA0575c"
/ Inote="PRA0575c"
/ Complement (join (201. .257,455. .586,748. .804))
complement (join (201. .257,455. .586,748. .804))
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/ Inote="PRA0575c"
/ Inote="PRA0575c"
/ Inote (SMALL:2019.18 SMALL:2019.18 SMALL:2019.18 SMALL:2019.18 SMALL:20117)
/ Go aa) fasta scores: E(): 1.3e-06, 39.68 id in 63 aa, and to Homo sapiens protein 15e1.1 Sell.1 SMALL:15E1 HUMAN (SMALL:493715) (76 aa) fasta scores: E(): 0.00046, 38% id in 50 aa, and to Mus musculus protein 15e1.1 15e1.1
/ Codon_start=1 in 50 aa"
/ Codon_start=1 in 50 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains possible signal sequence. Signal peptide predicted SignalP 2.0 HMM (Signal peptide probabilty 0.640, signal anchor probabilty 0.557) with cleavage site probability 0.504 between residues 27 and 28. ScanRegExp hit to PS00867, Carbamoyl-phosphate synthase subdomain signature 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MENRSKTISQNTIKAHVBANDECKEKKEKYLKCFNNWYKNNFLK
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NNNVDKIIITCTCLABIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNLNEILLEKNLDTIPGFKY
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LPMPLHMRNCSETFFKI VDIYKELFEKNGGVIHSFTDKEDI VHI I VQNYKNLY I GVNG
CSLKSLENI NAVKKI PLNILILETDAPWCGVKKTHASYEY I KDTYEKRAYTNLKKI KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDLTQACDDYYEDYQICVLNDLAKKGLGHLSNVEKEK"
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2990. 3276)
/gene="PFA0580c"
/note="PA0580c"
/note="synonym: MAL1P3.01"
2990. 3276))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="TatD-like deoxyribonuclease, putative"
'protein_id="CAD49076.1"
db_xref="G1:2377010"
'db_xref="UniProt/TrEMBL:081226"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /produc="hypothetical protein, conserved"
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                                                                                                           organism="Plasmodium falciparum 3D7"
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                                                                                                                                 'mol type="genomic DNA"
                                                                                                                                                                                        db_xref="taxon:36329"
chromosome="1"
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/gene="MAL1P3.02"
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                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19213 AATATATTTTATTTAATTTAATTTAAATA-ATTTAATTTAATTTTATTTTGTTTATTTTATT 39155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge (CBLO 1SA, UK On Dec 16, 1999 this sequence version replaced gi:5763807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INV 29-JAN-2003
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        275
                                                                                                                                                                                                                                                                                                                               456 CACAACAATTACACTCTCATCATTAAATTTAATTATTACCATAATTAAAATTGTGAGG 515
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                                                                                                                TICIATACTAATTATAAAATTCTGATCGGATTAGTGTGGTGTCAAAGTCAAGTCACATG
        AAIACTITIACITITITITITAAAAAGAAITICAATIGCGITITITICITAATITAGITITAA
                                                                                                                                                                                                                      576 CTTAITTCACTCCTAACAITAATCAITAACCCCAATTTTGAACTGTIATAATTTCTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barrell, B.G. Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Harris,D., Lawson,D., Quail,M., Rajandream,M., Hall,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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AL031746.9 GI:6594243
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PFMAL1P3/c
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                                                                                                                                      hit to vivax A-type 5.8S ribosomal percent id: 88.00 none"
26560. .27435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292
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CR391970.2 GI:46800726
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                  development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                           /product="ITS2 A-type"
/note="ribosomal operon internal transcribed spacer
                                                                                 'note="5.8S ribosomal exppressed in asexual stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 67970;
                                                                                                                                                                                                                                                                                              /product="288 ribosomal RNA (A-type)"
/note="288 rRNA expressed during asexual deve
complement(join(31966. 32476,32675. 32775))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                 expressed in asexual stage parasites"
27436. .31539
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; Score 112.8; DB 3;
50.9%; Pred. No. 5.2e-06;
iive 0; Mismatches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 ACATTAATCATTAACCCAATTTTGAACTGTTATAATTT
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                            /gene="mall_5.8srNA"
/product="5.8s ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                     /gene="MAL1P3.04"
                                                                                                                parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294; Conservative
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Best Local S
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CR391970/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ALC transporter, putative"
/product="ALC transporter, putative"
/product="ALC transporter, putative"
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/db_xref="GLA6358.1"
/db_xref="GLA6358LHBL.G9U0N4"
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/GDGLPNICKNPPDVPYZASKLEENLADIEVEDELFPTINLKGSNBTYLHCNSNDASE
KKVYNVYXHNILMSILKTFRFRIILIISFYILLSTILYTGKFRINGKNBNDASE
KKVYNVYXHNILMSILKTFRFRIILIISFYILLSTILKTTHKKSNBTHGCQKIPV
YISPLADFRVFGSGLVVMIMFPHLFPFALLHFYFHLFFTNLKVSNBNCHNCNN
NHLQNPDAFYNTYRKFSCOTEIDEISRDFLSIGKNASSSSSGIKNNKAUIDNNHFVI
KRFYTHKTGSNSVGIAIMELALYSANITERFLPSFLKSKTILYTROKRINDNHHVL
KEFKLIKMFWESPRFKYNSTNSTNSNBNFYCKILLSNVANFPRLSCOTSTINFNHHFVI
KREYFFYHKGNYTHKTRXNEDYNIVUDKTFLQNENITSHDDGTSHLKKHLKNVINTSHIHF
KKEFYHKGNYTHKTRXNEDYNIVUDKTFLQNENITSHDDGTSHLKKHLKNVINTNNINFN
KRYFFFYHKGNYTHKNINKNIINKQILSGLLKNUNDNHTKKILCTRUTKHNYINFN
KREYENIHNSSNSTMSNBNEFKEKKKNNBYIIKLENCSFGLSYDNKCDNHILLKNINFN
KREXENIHNSSNSTMSNBFREKKKKNINGYIIKLENCSFGLSYDNKCDNHILLKNINFN
KRNILEGNEFVHLINGSSCRAFFHS
NIRSMILEGNEFVHLIYDONSTRILDKDLINNKNISSYNNKKSKLUVNYNIPPNEN
RALVEHYIHHHKLCTPDYEKKLUQPNETILDKDLINNKNISSYNNKKSKLUVNYNIPPNEN
RALVEHYIHHKKLCTPDYEKKLUQPNETILDKDLINNKNISSYNNKKSKLUVNYNIPPNEN
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RALVEHYIHHHKLCTPDYEKKLUQPNETILDKOTTHENDNISSYNNKKSKLUVNYNIPPNEN
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RALVEHYIHHHKLCTPDYEKKLUQPNETILDKOTTHENDNISSYNNKKSKLUNYNIPPNEN
                                                                                                                                                             AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
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TUDYTR IKLEPEDELNHYKHSNRYIYERAFYVEKRESVYEETBOINKEKTKYY
KKEHWAKUNKONNANNANSNODHIN IN DANDHRAYADI NI CEPASTODS PTVSSIGNE
YTLDTYTSNNSDKEEIVKPLYYOTHEEPNKSSSMPFVKSSSNMINNPSNFKYEDNSSS
TYLORQYKYLEYTWYPQQVGFVLLTSVYI PMLISI STYDBIKFVETTMMSI ISKUNKEHSD
TILORQYNYLEYFYTLDYI ISLUTSGICFSMI IYGNITSBIKVHNNILYSILNAPLYIF
YNNNIGNI INRPIIIDISAPDYGFIKRIYKAFFIFFRENTISSLLIINPENYIF
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HYINNPRISYPFKWILNIWAGLYIKIFILLLTTIINHPHLYASGIIKLYKEKNYVRI
LSTLGYCISFSARLGVIIKFRLLCDYTHIEKEMCCVQRLEEFAKISKENENSMNKENEL
NYITYQTYKEKNENIESDKISALVEYKNYSLSSIINSQODESKKYGIKFENYVYSYY
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
                                                                                                                                   /translation="MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
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GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to Schizosaccharomyces pombe ATP-binding cassette transporter abc1 abc1 or spac9e9.12C SWALL:ABC1_SCHPO (SWALL:Q92337) (1427 aa) fasta scores: B(): 4.2e-08, 21.46 id in 1146 aa" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Putative ABC transporter
Pfam match to entry PF00005 ABC tran, ABC transporter,
score 45.00, E-value 1.7-09; HMMSmart hit to SM00382,
ATPages associated with a variety of cellular activities;
ScanRegExp hit to PS00211, ABC transporters family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="18s ribosomal RNA A-type"
'note="18s rRNA exppressed in asexual stage parasites"
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/note="ribosomal operon internal transcribed spacer 1
expressed in asexual stage parasites"
26439. .26559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                 xref="GOA:Q9U0NS"
xref="UniProt/TrEMBL:Q9U0NS"
     protein"
                                                                                                                                                                                                                                                               /note="Putative centromere"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                   /note="synonym: PFA0590w"
14884. .20352
/product="hypothetical p:
/protein_id="CAB63557.1"
/db_xref="GI:6594245"
                                                                                                                                                                                                                                                                                                   14884. .20352
/gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MAL1P3.03"
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Rattus norvegicus clone CH230-365P7, WORKING DRAFT SEQUENCE, 9 unordered pieces.
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Muray, D.Marie., Metaker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blairi, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AATTITITITITACCICCIGCCIAGATICGIAAAIACIAITGCATITATCICATITCAT 111
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                              Query Match
11.4%; Score 112.2; DB 2;
Best Local Similarity 54.0%; Pred. No. 5e-06;
Matches 318; Conservative 0; Mismatches 263;
                                      82495. .101952 /
/note="assembly_fragment:01300.0"
102053. .180861
'note="assembly_fragment:00011"
                                                                                                                                                              /note="assembly_fragment:01684"
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                                                                                                                                                                                                         Submitted (25-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquirises.
Zilab-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 27, 2004 this sequence version replaced gi:46559024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program (GAR4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 17704 bases at least Q40 Consensus quality: 177517 bases at least Q30 Consensus quality: 178043 bases at least Q20 Insert size: 180161; sum-of-contigs at least Q20 Quality coverage: 11.58x in Q20 bases; sum-of-contigs Quality coverage: 11.58x in Q20 bases; sum-of-contigs Quality coverage: 11.8x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 180861)
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53 102052: contig of 19458 bp in length
102052: gap of 100 bp
10052:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00026
fragment_chain:1"
4293. .15166
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79497. .82394
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15267. 33335
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56632. .79396
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ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: zfish-help@sanger.ac.uk
------ Project Information
Center project name: zK95F22
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/db_xref="taxon:7955"
/clone="bKEX-95F22"
/clone=lib="DanioKey"
1. .4192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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/organism="Danio rerio"
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                                                                                                                                                                       TITLE
JOURNAL
                                                                                              REFERENCE
                                                                                                                                         AUTHORS
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82040

349

231

81864

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a "working draft' sequence It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

47440: contig of 47440 bp in length 47540: gap of unknown length 230268: contig of 182728 bp in length 230368: gap of unknown length 254735: contig of 24367 bp in length 254835: gap of unknown length 275940: contig of 21105 bp in length 277252: contig of 11105 bp in length 277352: gap of unknown length 277352: gap of unknown length 278593: gap of unknown length 278593: gap of unknown length 282220: contig of 1141 bp in length 282220: contig of 3627 bp in length 282220: contig of 3627 bp in length

277253

276041

278494 278594

330269 54736

54836 275941

47441

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name:

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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cookrell, R., Cox, C., Coyle, M., Cree, A., D'Sousa, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, R., Dania, A., Bacotto, M., Daron, R., Dunn, A., Durnia, K., Duval, B., Eaves, K., Brander, S., Falley, M., Flagg, N., Porbes, L., Foster, M., Foster, P., Farsac, C. M., Gabra, M., Garcia, A., Garcia, A., Garcia, M., Garca, M., Garca, M., Gabrer, P., Fasser, C. M., Gabisi, A., Garcia, R., Garcia, A., Garcia, M., Garca, M., Gabrer, P., Fasser, C. M., Gabisi, A., Garcia, R., Garcia, A., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Gabrer, P., Fasser, C. M., Gabisi, A., Hawes, M., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Garcia, M., Gabrer, P., Haaland, M., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hanilton, S., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, J., Jackson, L., Jacckon, L., Jacoch, L., Jackson, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marin, M., Kargathy, S., Kelly, S., Kelly, S., Kally, S., Kally, S., Kally, S., Kally, S., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, 
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AUTHORS
TITLE
JOURNAL
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Direct Submission

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON VOV 6, 2002 this sequence version replaced gi:23097379.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

TITLE JOURNAL

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113 AFTTATTTAATTATTATATTATGGATAAAAATTCTAATACTTTACTTTTTTTAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 111.2; DB 2; Length 286208; 50.3%; Pred. No. 6.1e-06; tive 0; Mismatches 293; Indels 3; (
11 284049: contig of 1729 bp in length 10 286108: contig of 2059 bp in length. Location/Qualifiers
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Center: Baylor College of Medicine Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

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229479 173 229539 229596 229656 22971( 22977( 22983 22983 22983 22983 1110N 1110N 1110N 1110N 1110N	SOURCE Plasmodium falciparum 3D7  ORGANISM Plasmodium falciparum 3D7  EUKATYOTA; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  EUKATYOTA; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  REFERENCE AUTHORS Gardner, M. J., Hall, M., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Nelson, K., Salazberg, S.L., Craig, A., Kyes, S., Chan, MS., Nene, V., Shallom, S.J., Suh, B., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Ryes, S., Chan, MS., Nene, V., Shallom, S.J., Rairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., TTILE Genome sequence of the human malaria parasite Plasmodium falciparum JOURNAL Submitted (13-SE658)  1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 1. 258658 2. Location/Qualifiers Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 2085

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                                                                                                                                                                                                                             Query Match 11.2%; Score 110.2; DB 3; Length 258658; Best Local Similarity 51.4%; Pred. No. 8.3e-06; Matches 279; Conservative 0; Mismatches 263; Indels 1; ...
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Plasmodium falciparum chromosome 6, complete sequence; segment 2/5. CR382399 AL644505
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Conservative 0; Mismatches 300; Indels
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                                                                                                                                                                                                Submitted ("10-007-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 11, 2004 this sequence version replaced gi:54019775.
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 191191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 187123 bases at least Q40
Consensus quality: 187125 bases at least Q30
Consensus quality: 188211 bases at least Q20
Insert size: 190391; sum-of-contigs
Insert size: 199701; 0.8% error; agarose-fp
Quality coverage: 8.46x in Q20 bases; sum-of-contigs Quality
coverage: 8.18x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: zfish-help@sanger.ac.uk
------- Project Information
Center project name: zC223F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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Berriman,M., Pain,A., Hall,N., Atkin,R., Chillingworth,C.,
Doggett,J., Ormond,D., Sanders,M., Hayes,R., Hall,S., Quail,M. and
Barrell,B.G.
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Cherevach,I., Davis,P., Goodhead,I., Stevens,K., Mungall,K.,
Cherevach,I., Davis,P., Hall,N., Atkin,R., Chillingworth,C.,
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Barrell,B.G.
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Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
4 (bases 1 to 348174)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
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Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R.,
Hall, S., Quail, M. and Barrell, B.G.
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Direct Submission
Submitted (26-MAR-2004) P.falciparum Genome Sequencing Consortium,
The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CBIO 1SA, UK
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
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ETIYHHNLEHMNQDIDHRGHVDDIBNDFYYHGHGPMNKKHYMGKQNKFYNINEERRMV
LMKYRSLKIVAEDKWKLCLDFYSDIFVHVLDFASVLCNNIYDLRVIENVVLCFKTPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKNNDRGKKGEPRTLFYYEIYKKLFVYYECAINENERKNRKFLK
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NYMDEIIKCSIILNRNAYYVCTLFNDVYLKIEKSNIKNEIMKCTYICEVFKECIEKEN
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SMKSNHI SSNNNNNNNNNNNNNNNNNNNNNNNNNRSRYSI SNNQLAHIKFHKDLYKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCAAAGTCAAGTCACATGAATTTTTGTTGGAGAAAAAATAAAAATTAAAACACATTTTTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ATTCGTAAATACTATTGCATTTATCTCATTATTTAATTATTTAATTATATTATT
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Pred. No. 8.8e-06;
0; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="CAG25332.1"
/db_xref="G1:46361045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKADFGSSTEKIFKVLSSYGTSL"
20889. .39122
/locus_tag="PFF0445w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Asparagine-rich
MAL6P1.93"
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/locus_tag="PFF0445w"
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llarity 54.3%;
Conservative
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CR536620 169056 bp DNA linear HTG 27-JUN-2004
Danio rerio clone CH211-235C15, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                                          CCATAATTAAAATTGTGAGGACAATTATTTTTAATCTCACCCTCCATTAATGCATATTA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 27, 2004 this sequence version replaced g1:49256750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                436 TITITIAATITAAAATITCAGCACAACAATTACACTCTCATCATTAAAATITAATCTTATTA
                                        376 GATTAATTTATTATATATAATAATAAAACACATTTTTAATTAATGTTGTCAATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                        556 TIAATITITIGITICGATACTICTTATTICACTCCTAACATTAATCATT 602
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HTG; HTGS PHASE1; HTGS I
Danio rerIo (zebrafish)
Danio rerio
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CR536620/c
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BX247875 213093 bp DNA linear VRT 25-OCT-2003 Zebrafish DNA sequence from clone CH211-201N18, complete sequence.
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CH211-201N18"
/clone_lib="CHORI-211"
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                                                                                       BX247875.6 GI:37805637
                                                                                                                     Danio rerio (zebrafish)
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53.8%;
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                                                                                                                                                                                                                                                                                                                                     code: SC
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Best Local S
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                                                         DEFINITION
ACCESSION
                               BX247875/c
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTATTTAATTATTTTATATTTGGATAAAATTCTAATACTTTACTTTTTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 AAGAATTTATTTAATTTATTTTATTTTAGATAAAATTCTAATACTTTACTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 CAATTACACTCTCATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ATTTTTTTTTACCTCCTGCCTAGATTCGTAAATACTATTGCATTTATCTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 169056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
4 169056: contig of 43063 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                           11077. ... 95174
f.note="sasembly fragment:01332
fragment chain:1"
95275. ... 106934
f.note="sasembly fragment:00170
fragment chain:1"
107035. ... 125893
f.note="sasembly fragment:00340
fragment chain:1"
125994. ... 169056
                                                                                                          Score 109.6; DB 2
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                               /note="assembly fragment:00675
fragment_chain:1
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                                                         /mol_type="genomic DNA"
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/clone="CH211-235C15"
                                             /organism="Danio rerio"
                                                                                                       clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                              \mathtt{vector}_{\mathtt{z}} side:right"
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                             .169056
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSERCH; Tr:, TREMBL; WP:, WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish puc subclones occasionally display inconsistency over the length of monoucleotide A/T runs and conserved TA repeats. Where the this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
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Submitted (75-0CT-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 21, 2003 this sequence version replaced gi:37518258.
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CH211-201N18 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109.6; DB 5; Length
Pred. No. 1e-05;
0; Mismatches 244; Indels
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Danio rerio clone CH211-195G6, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                           442 AATTAAAATTTCAGCACAACAATTACACTCTCATCATTAAATTTAAT
                                                                                                                                                                                                                                                                                                                          552
                                                                                                                                                                                                                                                                                                                                                                                                    612
                                                                                     322 AGTCAAGTCACATGAATTTTGTTGGAGAAAAATAAAATTAAACACATTTTCGATTAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 10, 2004 this sequence version replaced g1:46879055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 197951)
                                                                                                                                                                                                                                                                                   TTACCATAATTAAAATTGTGAGGACAATTATTTTTTAATCTCACCCTCCATTAATGCATA
                                                                                                                                                                                                                                                                                                                                                               TAATITIAGTITITAATITCTATACTAATITATAAAATITCTGATCGGATTAGTGTGGTGTCAA
                                                                                                                                                                   TITATIATATATATAATAATAAACACATITITAATTAATGITGICAATAATATITITT
                                                                                                                                                                                                                                                                                                                                                                                                      TTATTAATTTTTGTTCGATACTTCTTATTTCACTCCTAACATTAATCATTAACCCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 193521 bases at least Q40
Consensus quality: 193982.bases at least Q40
Consensus quality: 194447 bases at least Q20
Insert size: 197051; aum.of.-contigs
Insert size: 201236; 3.3% error; agarose-fp
Quality coverage: 8.64x in Q20 bases; sum-of-contigs Quality
coverage: 8.52x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR392243
CR392343.2 GI:54021699
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
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of PFWALBP1 from base 1200001 (ALB44507 Plasmodium falciparum 3D
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                                                                                                              163627 irtraakigtairirtatttaagtriraattaarigaarirattiattattata 163568
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                                                                           AAGAATITTAATITATITITATATITTAGATAAAAATITCTAATACTITTATTTTTT
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llarity 50.9%; Pred. No. 1.4e-05;
Conservative 0; Mismatches 273;
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Continuation {13 of 14)
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PFMAL8P1 0
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Baldwin, D., Bandaranakke, D., Barcher, M., Baca, R., Benahmed, F.,
Baldwin, D., Bandaranakke, D., Barcher, M., Barnstead, M., Benahmed, F.,
Cardenas, V., Carter, K., Cavazos, I., Casaar, H., Center, A.,
Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Boderich, D.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Dutzhin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gabisi, A., Ganta, A., Garday, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harrandez, R., Hines, S., Hladun, S.L., Hodgen, A., Hodgues, M.,
Harnandez, R., Hines, S., Hladun, S.L., Hodgen, A., Hodgues, M.,
Harnandez, R., Jang, H., Vohnson, R., Johnson, R., Johnson, R.,
Jackson, L., Jacob, L., Jang, H., Lawis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., Longacre, S., Lopez, J.,
                                                                                                                                              177116 TTANATNNNAAATTTATTATTTTATNTTAATTTTANTTTTAATATATATTTTANAATTTTA 177057
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Rattus norvegicus clone CH230-61K4, WORKING DRAFT SEQUENCE, 4
unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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AC111404.5 GI:30579008
HTG; HTGS_PHASE1; HTGS_DRAFT; Exattus norvegicus (Norway rat)
Rattus norvegicus
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 109.2; DB 2; Length 197951; 46.5%; Pred. No. 1.2e-05; tive 0; Mismatches 318; Indels 0;
                                                                                                        contig of 16219 bp in length gap of 100 bp contig of 3448 bp in length gap of 100 bp contig of 26669 bp in length contig of 9744 bp in length contig of 9744 bp in length gap of 100 bp contig of 48244 bp in length gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp gap of 100 bp
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gap of 100 bp
contig of 52024 bp in length
gap of 100 bp
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4 182733: contig of 4910 bp in length

14 182833: gap of 100 bp

14 193584: contig of 10751 bp in length

15 193684: gap of 100 bp

17 193584: gap of 100 bp

18 193684: gap of 100 bp

18 193951: contig of 4267 bp in length.

19 Location/Qualifiers
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/note="assembly fragment:00222
fragment chain:2"
56481 .104724
/note="assembly fragment:02199
fragment chain:2"
104825 .125599
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1. .16219
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/note="assembly_fragment:00035
fragment_chain:1"
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gragment_chain:2
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ragment_chain:2"
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Matches 276; Conservative
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Litert Submission.

Submitted (13-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:24819049.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence in the feature
Loreneuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Manguua, P., Martin, R., Martinaz, B., Manguua, P., Martin, R., Martinaz, B., Manguua, P., Martin, R., Martinaz, B., Milosavijevic, A., Milos, M. Milos, J., Moore, S., Milosavijevic, A., Milos, M., Murphy, M., Nair, L., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Naackelemeh, O., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Poindexters, A., Popovic, D., Primus, B., Pui, L.-L., Puazo, M., Quiroz, J., Rachill, E., Reves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, M., Riggs, P., Reilly, B., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sanders, W., Savery, G., Scherer, S., Sorcile, K., Sasi, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, R., Weik, K., Weiker, R., Wang, J., Waight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinsten, G. and Gibbs, R.A. Shith, D.R., Smith, H.O., N. Weinsten, B., Smith, D.R., Smith, R., Smith, D.R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., Smith, R., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Atlas 3.0;
Consensus quality: 217670 bases at least Q40
Consensus quality: 219537 bases at least Q30
Estimated insert size: 231456; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
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Center: Baylor College of Medicine
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Rat Genome Sequencing Consortium.
Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 CACATTTTTATTTTAATGTTGTCAATAATATTTTTTAAAATTTCAGCACAACAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATCTCACCCTCCATTAATGCATATTATTAATTTTTTGTTCGATACTTCTTATTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGAATTTATTTAATTATTTTATTTTAGATAAAAATTCTA-----ATACTTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 TTATAAAAATTCTGATCGGATTAGTGTGTGTCAAAGTCAAGTCACATGAATTTTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 CACTCTCATCATTAAATTTTAATCTTATTACCATAATTAAAATTGTGAGGACAATTATTTT
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arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                          Length 246611;
                                                                                                     241059: contig of 241059 bp in length 242159: gap of unknown length 242345: contig of 1186 bp in length 242445: gap of unknown length 243601: contig of 1156 bp in length 24301: gap of unknown length 24611: contig of 2910 bp in length.
                                                                                                       241059 bp in length
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.1%; Score 109.2; DB 2; Length Best Local Similarity 51.3%; Pred. No. 1.1e-05; Matches 307; Conservative 0; Mismatches 284; Indels
                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
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US-09-949-016-146135
US-09-949-016-146403
US-09-949-016-146404
US-08-998-416-186
US-09-949-016-12699
US-09-949-016-12699
US-09-949-016-176490
US-09-949-016-176490
US-09-949-016-176490
US-09-949-016-176490
US-09-949-016-176490
US-09-949-016-162840
US-09-949-016-153480
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US-09-949-016-15350
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10.3%; Score 101.8; DB 4;
Best Local Similarity 48.1%; Pred. No. 2.6e-10;
Matches 286; Conservative 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gequence 1357, Application US/09902540

Facent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Miegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Seq.

FILE REFERENCE: 38-10(15849) B.

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1357
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OTHER INFORMATION: unsure at
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FARENTAL INCORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR                                                                  47953 ATAİTAİGTAİAATAİATAİAAATCCCCAİACTACGİAİACATGİAİACATATİTAİĞIC 47894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15129, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
NAME/TON: (1)...(55886)
OTHER INFORMATION: n = A,T,C or G
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Matches 257; Conservative
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ORGANISM: Human
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US-09-449-016-13504/c

US-09-449-016-13504, Application US/09949016

Sequence 13504, Application US/09949016

Return 0: 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOU1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FBELSEQ for Windows Version 4.0

LENGTH: 59519
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ATAAAAATTAAACACATTTTTCGATTAAATTTATATATAATAAAAATAAAACACATTT
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Pred. No. 6.4e-08;
0; Mismatches 313; Indels 3;
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Best Local Similarity 48.8
Matches 301; Conservative
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RESULT 5
US-09-349-016-15852/c
; Sequence 15852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, US CASAGE et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WINDER: US/09/949,016
; CURRENT PILLING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PILLING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILLING DATE: 2000-01-03
; PRIOR PILLING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SCOFTWARE: PASESEQ for Windows Version 4.0
; SEQ ID NO IS 207012
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| LOCATION: (1)...(205044)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852
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Best Local Similarity 50.5%;
Matches 265; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 205044
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Sequence 15851, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15851

LENGTH: 205044
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    5053 AATCTTATTTTATATATATTTTATATATATATAAAATCTTATTTTATATATATATATAT 4994
                                                                                    339 TITGITGGAGAAAAAAAAATTAAAACACAITITICGAITAATTITATATATATAT 398
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                                              ATATATAATATATAAAACACATTTTTAATTTTAATGTTGTCAATAATATTTTTTAATAA
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Pred. No. 1.8e-07;
0; Mismatches 258; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851
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Best Local Similarity 50.5%;
Matches 265; Conservative (
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LOCATION: (1)...(20504
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US-09-949-016-15851/c
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ORGANISM: Human
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US-09-949-016-15863/C

US-09-949-016-15863, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PSELSEQ for Windows Version 4.0

SEG ID NO 19853

LENGTH: 205044
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ACTITITITIAAAAAGAATTIATTIAAATAATTATTIATTITAGATAAAAATTCTAATA
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                                                         AACAATTACACTCTCATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACA
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Pred. No. 1.8e-07;
0; Mismatches 258; Indels 2;
                                                                                                                                         519 ATTATTTTTAATCTCACCCTCCATTAATGCATATTAATTTT 563
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 50.5%;
Matches 265; Conservative
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ORGANISM: Human
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Sequence 12387, Application US/09949016
; Sequence 12339
; Batent No. 681233
; Generat. INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    CURRENT APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
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AACAATTACACTCTCATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACA
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                                                                                                                                                                                                           Query Match
9.0%; Score 88.2; DB 4; Length 2
Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels
                                                                                                                                                  ATTATTTTTAATCTCACCCTCCATTAATGCATATTAATTTT
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NAME/KEY: misc_feature
LOCATION: (1)...(223471)
OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-12387/c
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; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725
                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (1)... (22347
                                                  US-09-949-016-12725/c
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ORGANISM: Human
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                                        519 ATTATTTTTAATCTCACCCTCCATTAATGCATATTATTAATTTT 563
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Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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Sequence 12725, Application US/09949016
Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171599 TCATGITTCATAGATAGGGGTCAATTCCTCATTTAAATATATTCAAATATAATATTT
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                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-06
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASSES OF WINDOWS VERSION 4.0
SOFTWARE: PASSES OF WINDOWS VERSION 4.0
SOFTWARE: 223471
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; ANTI-SENSE:
US-08-487-826B-13
               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                    STATE: CA
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             Sequence 17369, Application US/09949016

Sequence 17369, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICAMT: VENTER, J. Craig et al.

APPLICAMT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR PILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHAMER: FEBSEBE FOR WINDOWS VERSION 4.0
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Best Local Similarity 49.9%;
Matches 275; Conservative (
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ORGANISM: Human
RESULT 10
US-09-949-016-17369
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RESULT 11 US-08-487-826B-13/C

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APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEB: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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Pred. No. 2.2e-07;
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8.8%; Score 87; DB 2; Length 191

Best Local Similarity 50.1%; Pred. No. 2.2e-07;

Matches 252; Conservative 0; Mismatches 240; Indels
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PILLING DATE: 10-SEP-1993
CLASSIFICATION: 435
GCLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFREENCE/DOCKET NUMBER: 19121.001CP1
TELECOMMUNICATION INFORMATION:
TELEFONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDENNESS: single
Sequence 13, Application US/08487826B Patent No. 5993827
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                               Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
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Sequence 15940, Application US/09949016

Sequence 15940, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOCTAMER FEASTER FASTER FOR WINDOWS VERSION 4.0

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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8.7%; Score 85.8; DB 4; 1
Best Local Similarity 51.0%; Pred. No. 4.9e-07;
Matches 281; Conservative 0; Mismatches 262;
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OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc feature
LOCATION: (1)...(19156
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US-09-949-016-15940/c
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
FURBENT FILING DATE: 2000-10-414
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                          ----AAATTTTTTTTATAT 15470
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Pred. No. 4.9e-07;
                                                                                 15518 CTCCTTTTTTTTTTTTTTTTTTTATTTAAT
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US-09-949-016-12776/c
; Sequence 12776, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                               538 CTCCATTAATGCATATTAAT 560
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.0%;
Matches 281; Conservative
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LOCATION: (1)...(18716)
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ORGANISM: Human
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51.1%;
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Best Local Similarity 51.1
Matches 247; Conservative
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CRGANISM: Human
US-09-949-016-12386
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US-09-949-016-12386
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US-09-902-540-1280/c

is aguence 1280, Application US/09902540

patent No. 683347

GENERAL INFORMATION:
APPLICANT: Gldman, Barry S.
APPLICANT: Alinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Misgand, Roger C.
APPLICANT: BLOOK INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1280

LENGTH: 1039
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Pred. No. 4.7e-07;
0; Mismatches 312; Indels 2
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| DOCATION: (1)..(1039)

| OTHER INCRMATION: unsure at all n locations

US-09-902-540-1280
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Best Local Similarity 47.4%;
Matches 283; Conservative
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Sequence 12386, Application US/09949016
; Sequence 12386, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPRENCE: CLO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FRASEQ for Windows Version 4.0
; SEQ ID NO 12386
; MANDEL OF SEASED FOR MINDOWS NAMED IN NAME OF SEX OF MINDOWS NAMED IN NAMED OF SEX OF MINDOWS NAMED IN NAMED OF SEX OF MINDOWS NAMED IN NAMED OF SEX OF MINDOWS NAMED IN NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF MINDOWS NAMED OF SEX OF 
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                                                                          CICACCCICCATIAAIGCATATIAAITITITIGITGGATACTICTIAITICACTCCIAA 591
531
                                                                                                                                                                                                                                           TIABAATIGIGAGGACAAITATITITAAICICACCCICCAITAAIGCAIAITAAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251787 ATTTAATTTAATTATATATTAATTTAATTTAATTATATTAATTTAATTTAATTTAA
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Pred. No. 1e-06;
0; Mismatches 233; Indels
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562 TTT 564 |||| 252087 TTT 252089

Search completed: March 15, 2005, 02:00:37 Job time : 214 secs

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March 15, 2005, 01:02:26 ; Search time 607 Seconds
  (without alignments)
  9652.881 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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985
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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	Description	Sequence 386, App	Sequence 240, App	GENERAL INFORMATI	Sequence 10, Appl	Sequence 10, Appl	Sequence 386, App	Sequence 240, App	Sequence 132399,	Sequence 1, Appli	Sequence 2128, Ap	Sequence 299, App
	OI.	US-10-473-126-386	US-10-473-126-240	US-10-211-179-11	US-10-094-240-10	US-10-056-405-10	US-10-473-126-386	US-10-473-126-240	US-10-425-115-132399	US-10-312-841-1	US-10-311-455-2128	US-10-311-455-299
	80	18	18	17	14	16	18	18	18	16	15	12
	e Match Length DB I	8056	8056	158001	4985	4985	8056	8056	1130	3673778	15548	6109
ouery	Match	.10.9	10.7	10.6	10.6	10.6	10.3	10.2	9.9	9.8	9.8	7.6
	Score	107.4	105.8	104.8	104.4	104.4	101.6	100	97.8	96.4	96.2	95.4
Result	No.	1	7	о С	4	2	φ υ	0 7	ω υ	o	10	11

SUMMARIES

Semience 33, Appl	. 0	Sequence 11234, A	Sequence 5746, Ap			Sequence 330, App			373,	17271	7	32,	2331			Sequence 240, App		Sequence 2180, Ap	Sequence 1280, Ap	227,	945,	339,	81106	61	313,	513,	461,	1646,	Sequence 7699, Ap		ť	4	1734,
11S-10-221-813	US-10-311-455-952	JS-09-960-352-11234 {	US-10-741-601-5746	US-10-741-600-17905	US-10-741-600-17721	US-10-311-455-330	US-10-437-963-21828	US-10-257-166-13	US-10-311-455-373	US-10-425-115-172717	US-10-	US-10-433-793-32	US-10-311-455-2331	US-10-221-714A-252	US-10-425-115-120013	US-10-311-455-240	US-10-363-345A-2179	US-10-363-345A-2180	US-10-311-455-1280	US-10-311-455-227	US-10-311-455-945	US-10-473-126-339	US-10-425-115-81106	US-10-221-613-61	US-10-221-714A-313	US-10-221-714A-513	US-10-221-714A-461	US-10-311-455-1646	US-10-021-323-7699	US-10-311-455-986	US-10-311-455-1271	-71	US-10-311-455-1734
7	15	6	18	19	19	15	18	11	15	18	16	18	15	11	18	15	18	18	15	15	12		18		11	11		15		15	15	11	12
9019	6963	419	49979	49979	119036	9642	591	6216	7167	1243	3673778	6048	12237	7814	1062	6419	778	778	6175	18154	6145	3683	1004	5768	6286	61020	6292	12142	520	7597	12025	7442	7851
0	. 0	9.6	9.5	9.5	9.5	9.5	9.4	9.3	9.3	m.	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.0	9.0	9.0	9.0	0.0	9.0	9.0	8 6.	8.9	8.9	8.9	8.9
4 70	94.6	94.4	94	94	94	93.6	92.2	91.8	91.8	91.6	91.6	91.2	91.2	8.06	90.6	90.6	90.2	90.2	90.2	90	9.68	68	88.4	88.4	88.4	88.4	88.2	88.2	88	87.8	87.6	87.4	87.2
	13	14	12	16	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT 1 US-10-473 Podiucity Publice GENERAL TITLE TITLE FILE FURBER CURRER CURRER NUMBER NUMBER TYPE TYPE TYPE TYPE TYPE TYPE TYPE TYPE	RESULT 1  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386  18-10-473-126-386
Query Match Best Local Matches 30	Query Match 10.9%; Score 107.4; DB 18; Length 8056; Best Local Similarity 51.1%; Pred. No. 1.3e-05; Matches 305; Conservative 0; Mismatches 286; Indels 6; Gaps 2;
\$ 8 8	52 AATTITTATTITACCICCIGCGIAGATICGIAAATACTATIGCATTIATCICATTICAT 111 
රු දු	112 TATTTATTTAATTATTTATATTATGATAAAAATTCTAATACTTTACTTTTTTAA 171 
<i>\</i> 0	172 AAAGAATTTATTTAATTATTTATATATAAAAAATTCTAATACTTTACTTTTT 231

Db 293 ATTTTTTTAAAATTATTTTTAAAAAATTAATTAATAAAAA	RESULT 3 US-10-211-179-11/c US-10-211-179-11/c ; GENERAL INFORMATION: ; APPLICANT: Nicholas M. Dean ; APPLICANT: Nicholas M. Dobie ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI ; FILE REPERENCE: PFS-0011 ; CURRENT APPLICATION NUMBER: US/10/211,179 ; CURRENT FILING DATE: 2002-08-01 ; NUMBER OF SEQ ID NOS: 119 ; OTHER INFORMATION: n = a, t, c, or g US-10-211-179-11	Query Match         10.6%;         Score 104.8;         DB 17;         Length 158001;           Best Local Similarity 49.7%;         Pred. No. 6.2e-05;         Adaches 297;         Longervative 0;         Adaches 297;         Indels 4;         Gaps 1;           Qy         52 AATTTTTTATTTTATTTTATTTTATTTTATTTTATATTTT	22632 22632 288 22572 348 22512 22512 22452 22452 22332
Db 173 TATTATTTTTTAATTATTAATTATTATTATTATAATTTTT	Oy 528 TAATCTCACCCTCCATTAATGATTTTGTTGATACTTTTTCACTC 587  Db 533 TAAAATTAAAATTATATATATTATTAAAATTTTTGTTCAATATTTTCACTC 587  Oy 588 CTAACATTAATCATTAATCATTTTTAAAATTTTTTAAAATTTTTAAAATTTTTAAATTTT	FUBLICACION NO. OSCULOSARIA INFORMATION: APPLICANT: Epigenomics AG TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell TITLE OF INVENTION: MADDITION NUMBER: US/10/473,126 CURRENT APPLICANTO NOS: 1258 CURRENT APPLICANTO NOS: 1258 CURRENT ABOS TYPE: DNA ORGANISM: Artificial Sequence FEATURE: FEATURE: CURRENT INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-240	Query Match Best Local Similarity 50.9%; Pred. No. 2.2e-05; Matches 304; Conservative 0; Mismatches 287; Indels 6; Gaps 2;  Oy 52 AATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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2678 ATTAATTATTATTATTATTATTATTATTGTTATTCATTATTATTATACATT--ATTATCAT 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ATTTATCTCATTTCATTATTTAATTATTTTATATTATTTTTGGATAAAATTCTAATA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF FILLE REFERENCE: NB289
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHTIN VET. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 TTCTATACTAATTATAAAATTCTGATCGGATTAGTGTGGTGTCAAAGTCAAGTCACATG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 AATTTTGTTGGAGAAAAAAAAAATTAAACACATTTTTCGATTAATTTATTATATAT 395
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                                           588 CTAACATTAATCATTAACCCAATTTTGAACTGTTATAATTTCTTAACTTATTCACTAT 645
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%
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104.4; DB 14; Length
Pred. No. 3e-05;
0; Mismatches 266; Indels
                                                                                                          RESULT 4
US-10-094-240-10
Sequence 10, Application US/10094240
Publication No. US20030082637A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.7%;
Matches 276; Conservative (
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2916 TATT 2919
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US-10-056-405-10

Sequence 10, Application US/10056405

Publication No. US20030166013A1

GENERAL INFORMATION:

APPLICANT: ZMIEBEL, LAURENCE J.

TITLE OF INVENTION: WOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METH

TITLE OF INVENTION: USE THEREOF

TITLE REFERENCE: N7841

CURRENT APPLICATION NUMBER: US/10/056,405

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1
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Pred. No. 3e-05;
0; Mismatches 266; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.7%;
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Anopheles gambiae
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US-10-473-126-386/c
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LENGTH: 4985
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Sequence 12299, Application US/10425115
Sequence 12299, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 132399
LENGTH: 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ATTITITIATITITACCICCTGCCTAGATICGTAAATACTATIGCATITATCTCATITICATI
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                                                                                                             Length 8056;
                                                                                                                                             Indels
                                                                                                          Score 100; DB 18;
Pred. No. 0.00014;
0; Mismatches 297;
                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                            Query Match
Best Local Similarity 49.2%;
Matches 290; Conservative
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
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   LENGTH: 8056
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Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT APPLICATION NUMBER: US/10/473,126
SEQ ID NOS: 1258
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
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, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386
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Pred. No. 8.3e-05;
                                                                   CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 49.4%;
Matches 291; Conservative
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US-10-473-126-240/c
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9.8%; Score 96.2; DB 15;
Best Local Similarity 53.7%; Pred. No. 0.00054;
Matches 267; Conservative 0; Mismatches 223;
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Publication No. US20030186277A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841

CURRENT FILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 1

LENGTH: 3673778
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                                                                                        Length 1130;
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Best Local Similarity 50.4%; Pred. No. 0.00017;
Matches 263; Conservative 0; Mismatches 258;
                             FEATURE: OTHER INFORMATION: Clone ID: MRT4577_52232C.1
                  n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
LOCATION: (1)..(1130)
OTHER INFORMATION: unsure at
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Best Local Similarity 50.3
Matches 291; Conservative
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LOCATION: (3294164)
                                               , OTHER INFORMATION
US-10-425-115-132399
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| Sequence 33, Application US/10221613
| Publication No. US20040029123A1
| GENERAL INFORMATION:
| APPLICANT: OLEK, ALexander |
| APPLICANT: PIPENBOCK, Christian |
| APPLICANT: BERLIN, Kurt |
| TITE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle |
| TITE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle |
| TITE OF INVENTION: Diagnosis of Diseases Price |
| TITE OF INVENTION: DIAGNOSIS |
| CURRENT APPLICATION NUMBER: US/10/221,613 |
| CURRENT APPLICATION NUMBER: PCT/EP01/02945 |
| DE 100194058 |
| DE 10019173 |
| DE 10019173 |
| DE 10043826.1 |
| PRIOR FILING DATE: 2001-03-15 |
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NUMBER OF SEQ ID NOS:
SEQ ID NO 33
LENGTH: 6109
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; Sequence 299, Application US/10311455
; Publication No. US20030143606A1
; Publication No. US20030143606A1
; GENERAL INFORMATION:
    APPLICANT: OLEK, ABexander
; APPLICANT: PIERENROCK, Christian
APPLICANT: BERLIN, Kurt
    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by FILE REPRINCE: 2002-12-16
    PRIOR PRILING DATE: 2002-12-16
    PRIOR FILING DATE: 2000-06-30
    PRIOR FILING DATE: 2000-06-30
    PRIOR PLING DATE: 2000-06-30
    PRIOR PLING DATE: 2000-09-01
    NUMBER OF SEQ ID NOS: 2424
    SEQ ID NO 299
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        TATTGCATTTATCTCATTTCATTTATTTAATTATTTATATTTGGATAAAATT
                                                    TCACATGAATTTTTGGAGAAAAATAAAATTAAAACACATTTTTGGATTAATTTATTA
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9.7%; Score 95.4; DB 15;
Best Local Similarity 49.7%; Pred. No. 0.00055;
Matches 296; Conservative 0; Mismatches 296;
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| LOCATION: 214, 2796..2797, 4347
| OTHER INFORMATION: n is a or g or c or US-10-311-455-299
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ORGANISM: Artificial Sequence
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byat., John C.
TITLE CALL SHIP STATE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCHER, 1010-298).C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
ESEQ ID NO 11234
LENGTH: 419
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; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
US-09-960-352-11234
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                    ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-952
                                                                                Score 94.6; DB 15;
Pred. No. 0.00074;
0; Mismatches 289;
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Pred. No. 0.00039;
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Sequence 25.2, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: BIRLIN, Kurt

TITLE OF INVENTION: Disposis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: Disposis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: DATE: 2002-12-16

PRIOR PELICANTON NUMBER: DC1/0311,455

CURRENT FILING DATE: 2000-07-02

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 2424

SEQ ID NOS: 2424
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                                                                                     Length 6109;
                                                                                Query Match 9.7%; Score 95.4; DB 17; Length Best Local Similarity 49.7%; Pred. No. 0.00055; Matches 296; Conservative 0; Mismatches 296; Indels
                 (214, 2796..2797, 4347)
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NAME/KEY: unsure
LOCATION: (214,
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US-10-311-455-952
                          ; LOCATION: (2)
US-10-221-613-33
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// LOCATION: (1)...(49979)
// OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5746
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Sequence 5746, Application US/10741601

PUBLICALION NO. USCO40166519A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01500

CURRENT FILING DATE: 2003-12-22

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NUMBER OF SEQ ID NOS: 26415

SEQ ID NO STACE

TENOMALY OF SEQ ID NOS: 24415

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Best Local Similarity 51.8%; Pred. No. 0.0015;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AL069706 Drosophil AL064091 Drosophil AL069706 Drosophil AG381852 Mus muscu			AG486400 Mus muscu ALI74271 Tetraodon CG754663 P050-2-60 CL076889 CH216-151 CL068807 CH216-115 CL479576 SAIL 308 AG350209 Mus muscu CG749499 P043-4-A0 CR734084 Tetraodon CG757503 P052-4-C0
SUMMARIES	CNSOOEVL CNSOO3BD CNSOOEVL AG381852	CNS016CO AG396166 CL033318 BH177277	CNS 0 7 JUX CNS 0 0 E O 7 AG 3 8 6 9 8 1 BQ 1 5 1 1 8 7 CNS 0 6 0 I CG 7 5 3 0 8 3	AG466400 CNS012GM CG754863 CL078589 CL0785807 CL078576 AG350209 CG744999 CG734084
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BY720774 BY720774 CB207771 AGENCOURT AL064089 Drosophil CL128786 ISB1-95C2 AG43010 Mus muscu BE577630 mm57.550. CL118721 ISB1-7248 CL135318 ISB1-106F AG321256 Mus muscu CL104752 ISB1-4111 AG430338 Mus muscu AL063921 Drosophil CL077121 CH216-143 CL087333 ISB1-9A17 CG749728 P044-1-CO AG39098 Mus muscu CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143 CL077082 CH216-143	ALIGNMENTS  melanogaster genome survey sequence T7 end of BAC: if RPCI-98 library from Drosophila melanogaster (fruit  GI:4949849  melanogaster (fruit fly)  melanogaster Metazca; Arthropoda; Hexapoda; Insecta; Pterygota; indopterygota; Drosophila. i. Drosophilidae; Drosophila. i. to 1101)	Genoscope.  Joinect Submission  Direct Submission  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila and was constructed by partial ECORI digestion of Drosophila back clone strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be	<pre>ialo.edu/drosophila_bac.htm. melanogaster" '" 7.5e-11;</pre> Length 1101;
6 BY720774 6 CB207771 9 CNS003BB 10.12876 8 B2577630 8 B2577630 8 CL1185318 9 CL1185318 9 CL1017121 9 CL1087333 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728 9 CG749728	ALIGNMENTS  1101 bp aster genome surv 98 library from D ey sequence. 9849 aster (fruit fly) aster 7, Arthropoda; Hex y, Arthropoda; Hex philidae; Drosoph	1999) Genoscope cedex - FRANCE ope.cns.fr) ope.cns.fr) ope.cns.fr) ope.cns.fr) the Berkeley D ucting a physic e using these B /www.fruitfly.o ibrary was prep Pieter de Jong' the Roswell pa named RPCI-98 Drosophila DNA c cn bw sp, the es A more deta ndividual BNC c ication from th	http://bacpac.med.buffal Location/Qualifiers 1. 1101 /organism="Drosophila me /mol_type="genomic DNA" /db_xref="taxon:727" /clone="BACR29B23" /clone lib="RPCI-98" /note="end: T7" 13.4%; Score 131.6
11.1 939 11.1 1005 11.0 1127 11.0 1227 11.0 1268 11.0 1268 11.0 1268 11.0 1268 11.0 1291 11.0 1291 11.0 1291 10.9 1210 10.9 1210 10.9 1314 10.9 1314	CNSOOEVL Drosophila melanogaster Ely, genomic survey ser AL069706 AL069706.1 GI:4949849 GSS. Drosophila melanogaster Drosophila melanogaster Drosophila melanogaster Drosophila melanogaster Bukaryote; Metazoa; Artl Nooptera; Endopterygota Ephydroidea; Drosophilia	Direct Submission Submitted (102-JUN-1 BP 191 91006 EVRY BP 191 91006 EVRY Determination of the collaboration with the BDGP is construct melanogaster BAC is melanogaster BAC is Aaron Mammoser in E Cancer Genetics at Cancer Genetics at Cancer Genetics at Aaron Genetics at Cancer Genetics at Cancer Genetics at An and Cancer Genetics at ECRI dispestion of isogenic strain y2, pl and EST librarie Filters for hybridia	found at http://bacg location/Qi urce
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Drosophila melanogaster genome survey sequence T7 end of BAC:
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Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/mol_type="genomic DNA"
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/clone="BACR08K08"
                                                                                                                                                                                                                                                                      /clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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                                                                          TITAAAAAGAATITCAATIGCGITTITTTTTTTTAATITTAGITTTTAATTCTAATTAATA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                     274;
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Drosophila melanogaster
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.jp, Wit.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                      AG381852 1352 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-192A15.T7, genomic survey
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                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BAC end Sequences of Library MSMg01
Unpublished
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Direct Submission
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 4.5e-09;
0; Mismatches 294; Indels
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/organism="Mus musculus molossinus"
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-192A15.T7"
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                                                                                                                                                                                                                                                                          Direct Submission.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Discophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Goeogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and bw to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                              melanogaster (fruit fly)
£1y), genomic survey sequence.
AL069706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="BACR29B23"
/clone lib="RPCI-98"
/note="end : T7"
                                                                                            Drosophila melanogaster
Drosophila melanogaster
                                            AL069706.1 GI:4949849
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                                           174 AGAATTTATTTAATTATTTTATTTTTAGATAAAAATTCTAATACTTTACTTTTTT
                86; Mismatches 164;
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Determination of this BAC-end sequence was carried out as part of collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106578
AL106578.1 GI:5622626
                                                                     TTTTATTTAATGTTGTCAATAATATTTTTTTAATTTAAAATTTCAGCACAACAATTACACTC
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                                     847 TINTITITATTTGEAATATTTTATATTTTAGTTTTAGTTTTATTTTTTT
      AAAGAATTTATTTAATTATTTTATTTTAGATAAAATTTCTAATACTTTACTTTTTT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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db_xref="taxon:7227"
clone="BACN15E04"
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/plasmid="pBeloBAC11"
/note="end : T7"
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170] Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyada, Tsukuba, 305-0074 Japan Bhone: 81-288-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                   AG196166 1441 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSWg01-216D06.TJ, genomic survey
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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BAC end Sequences of Library MSMg01
474 ATCATTAAATTTAATCTTATTACCATAATTAAAATTGTGAGGACAATTATTTT
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/mol_type="genomic DNA"
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/sex="male"
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Xenopus tropicalis
Bukaryots in Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryots as Arachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases i to 1275)
Xremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, B. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
                                                                                                                                                              639 TITTITITATITATATATITITITITATITITITATATITITAAATITITATATITITAT
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                                                                                                            Length 1441;
                                                     /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                         Score 115; DB 9; Length 14
Pred. No. 2.6e-08;
0; Mismatches 275; Indels
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/db_xref="taxon:57486"
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Matches 280; Conservative
                                          /sex="male"
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886 bp DNA linear GSS 19-OCT-2001
008 L 22-rev SmBAC1 Schistosoma mansoni genomic clone 008L22 5',
genomic survey sequence.
BH177277 GI:16275873
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Washington University School of Medicine Email: submissions@watson.wustl.edu Insatz Length: 175000 Std Error: 0.00 Seg primer: Sp6 ATTAGGTGACACTATAG Class: BAC ends High quality sequence start: 40 High quality sequence stop: 194.
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AL614235.1 GI:16027459
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Schistosoma mansoni
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Matches
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/lab_host="Biomphalaria glabrata"
/lab_host="Biomphalaria glabrata"
/clone_libe="SmBAC1"
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."
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Contact: Pierce RJ
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Incetiut Pasteur de Lille
Incetiut Pasteur de Lille
I rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 2087783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID-DGOAAROOBFIIBPI
Plate: 008 row: L. column: 22
Seq primer: M13 reverse primer
Class: BAC ends
High quality sequence stop: 886.
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                                                                                                                                                                                                                                                                                                                                                             /organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="Puerto-Rican"
                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:6183"
                                                                                                                                                                                                                                                                                                                                                                                                                  clone="008L22"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="mixed"
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Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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T3 end of clone 008DF11 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni.
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TITIAATTAAAATTICAGCACAACAATTACACTCTCATCATTAAATTIAATCTTATTACC
                                                      527 İKTİTAKAAAAAKWATTKKTKTWDKKKKARARATKKKKAKKAKTTKTİKİKAWWAİKTİTAT
                                                                                                                                                                                                                                             558 AATTITIGITCGATACTICITATTICACTCCTAACATTAATCATTAACCCAATTITGAAC
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Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
1 (bases 1 to 886)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Le Paslier, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., Loverde, P.T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library Genomics 65 (2), 87-94 (2000)
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44.9%; Pred. No. 3.5e-08;
iive 54; Mismatches 259;
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/mol_type="genomic DNA"
/strain="Puerto-Rican"
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/clone lib="SmBAC1"
/note="end : T3"
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GSS 03-JUN-2004
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Mus musculus molossinus DNA, clone:MSMg01-201G10.TJ, genomic survey
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Direct Submission
Bubmitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-chou,Tsurumi-Yu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL.http://hgp.gsc.riken.go.jp/,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
Unpublished
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                                                                                                                                                              Length 1101;
                                                                                                                                                      11.6%; Score 114; DB 9; Length 11
40.5%; Pred. No. 3.9e-08;
:ive 89; Mismatches 255; Indels
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    /clone_lib="RPCI-98"
/note="end : TET3"
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and menanogaster BAC library was prepared by Carutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's plant and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS00EO7 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
528
                                                                                                                         TTCTTAATTTAGTTTTAATTCTATACTAATTATAAAAATTCTGATCGGATTAGTGTGGTG 317
                                                                                                                                                                                                                                                                           TTAATTTATTATATATATAATAATATAAACACATTTTTATTTAATGTTGTCAATAATATT 437
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                                                                                                                                                                                                                                                                                                                        646 TAATAAAAWTTTTATAAAAWTATTTTTTTTTTTTTAAAAAT-TAWTTWATWAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can t found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophildae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 TTAAAAAATTAATSARSTTATSTASTRTAATTKS 314
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/db_xref="taxon:7227"
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RESULT 10 CNSO0EO7/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

COMMENT

source

FEATURES

561 595

Bell, C.J.,

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354 AIAAAAATTAAACACATTTTTCGATTAATTTATTATATATAATAATAAAACACATTT 413
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                                                                                                                                                                                                             Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J. Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf-library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ATTAAAATTATATATTATATTATTTTTTÄTTÄTTTTTTÄTATTTTAAAATAA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 ITATTTAATGTTGAATAATATTTTTAATTAAAATTTCAGCACAACAATTACACTCTC
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                                  NF048A07LF1F1050 Developing leaf Medicago truncatula cDNA clone
NF048A07LF 5', mRNA sequence.
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/clone lib="Developing leaf"
/note="Vector: Lambda Zap; Contains a mixture of
young, developing, mature and senescing leaves."
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                                                                                                                                                                                                                                                                                                               Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 224 6650
Fax: 580 224 6652
Bmail: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 112.8; DB 5; 50.7%; Pred. No. 6.3e-08; ive 0; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 839 Std Error: 0.00
Plate: 048 row: A column: 07
Seg primer: TCACACAGAAACAGCTATGAC.
                                                                                                                  Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db xref="taxon:3880"
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/tissue_type="leaf"
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                                                                                                                                    Medicago truncatula
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Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude. Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1542;
                                                                                                                                                                                                                                                                                                                                                                        /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 5.3e-08;
0; Mismatches 298; Indels
                                                                                                                                                                                                                                                   /organism="Mus musculus molossinus"
/mol type="genomic DNA"
/sub_species="m-1
                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:57486"
/clone="MSMg01-201G10.TJ"
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                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1896).
Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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                                                                                                                                         675 TITATITWSITIATIWITITWITIATIAAAITITITIAGAAAAITAAITASITITAI 734
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                                                                                                                                                                                                                                                                                       410 ATTTTTATTTAATGTTGTCAATAATATTTTTAATTAAAATTTCAGCACAACAATTACAC
    230 TITITAAAAAGAATITICAATIGCGTITITITITITAATITAGTITITAATITCIATAATIA
                                                   290 TAAAAATTCTGATCGGATTAGTGTGTGTCAAAGTCAAGTCACATGAATTTTGTTGGAGA
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Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Tel: 00497071601371
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
Class: BAC ends.
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22835951
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/clone_lib="Ppa_BcoRI_BAC_Library"
/note="The_library_was_generated_by
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Pred. No. 7.9e-08;
0; Mismatches 289;
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1. 1896
Arganism="Pristionchus pr/mol_type="genomic DNA"
| gtrain="California"
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ilarity 50.7%;
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Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr. - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Biffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Erosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp., the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK14U23 of RPCI-98 library from Drosophila melanogaster (fruit AL065624
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534 CACCCTCCATTAATGCATATTATTAATTTTTGTTCGATACTTCTTATTTCACTCCTAACA
                                                                                                                     110 ATTATTTATTTAATTATTTTTATTATTTTGGATAAAAATTCTAATACTTTACTTTTTTT
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebpydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 990)
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14J23"
/clone="BACR14J23"
/note="end: TET3"
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45.2%; Pred. No. 8.1e-08;
tive 31; Mismatches 288;
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:181-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
                                                                                                                                                                                                                                                                                                                                                                                                     AG486400 810 bp DNA linear GSS 04-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-382105.TJ, genomic survey
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                    tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                             organism="Mus musculus molossinus"
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
                                                                                                                                                                                                                                                                                                                                 11.3%; Score 111.6; DB 9;
llarity 48.8%; Pred. No. 9.7e-08;
Conservative 0; Mismatches 308;
                                                                                                                                                                                          /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-382105.TJ"
                                                                                                                                              Location/Qualifiers
                                                                                                : pBACe3.6
: EcoRI
                                                                                                                                                                                                                                                            /sex="male"
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